

EORI

TCCAGGCTTT AGTGAATTC CGATTAG TTCAATTTGT TAAAGACAGG ATCTCAGTAG 7740
AATAATATAA AGATTTTATT TAGTTTCCAG AAAAAGGGGG GATGAAAGA ^{IR} 7800
REFMLVCGD.ENV
TTGCTTAGCC TGTAGCCGC AGTAACGCCA TTTTGCAAGG CATGGAAAAA TACCAAAACCA 7920
AGATATAGAGA AGTTCAGATC AAGGGGGGGT ACAGGAAAC AGCTAACGTT GGGCCAAACA 7980
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCGGGGGGCC AAGAACAGAT GGTACCCGG 8040
GTTCCGGCCC GCGCGGGGGC CAAGAACAGA TGGTCCCCAG ATATGGCCCA ACCCTCAGCA 8100
GTTCTTTAG ACCCATCAGT TGTATCCAGG CTCCCCCAAG GACCTGAAT GACCTGTGC 8160
CTTATTGGAA TTAACCAATC AGCCTGCTTC TCGCTTCTGT TCGCGCGCTT CTGCTTCCCG 8220
AGCTCTATAA AAGAGCTCAG AACCCCTCAC ^{U3}
GGCCAGTCC TCCGATAGAC TGAGTCGCC GGTACCCGT ^{IR} ^{Kpn I} GATCCAATA AATCCTCTTG 60
CTGTTGCATC CGACTCGTGG TCTCGCTTT ^{U5} ^{IR} ^{Kpn I} CCTTGGGAGG GTCTCCTCAG AGTGATTGAC 120
TACCCGTCTC GGGGTCCTT CATTTGGGG CTCGTCCGG ^{IR} ^{Kpn I} ATCTGGAGAC CCCTGCCCG 180
GGACCACCGA CCCACCACCG GGAGGTAAGC TGGCCAGCAA TGTGTTCTGT ^{IR} ^{Kpn I} TCTGTCCATT 240
GTCCTGTGTC TTTGATTGAT TTTATGGCC TGTGTCGTGA CTAGTTGGCC ^{IR} ^{Kpn I} GACTAGATTG 300

FIGURE 1a

^{Bam HI}
└─┐
GTATCTGGCG GATCCGTGGT GGAACGACG AGTTCGAGAC ACCGGCGCG AACCTGGGA 360
GACGTCCAG GACTTCGGG GGCCATTTT GTGGCCGGC CAGAGTCGAA CCATCCCGAT 420
CGTTTGGAC TCCTTGGTC ACCCCCTTA GAGGAGGGT ATGTGTTCT GTAGGAGAC 480
AGAGGGCTAA AACGGTTTC GCGCCCTCT GAGTTTTCG TTTCGGTTG GAACCGAGC 540
CGCGCCGCG GTCTTGTCTG ⁹⁰⁰CTGCAGCATC GTCTGTGTGT GTCTGTGTGT GACTGTTTT 600
CTGTATTGT CTGAAACAT GGGCCAGGCT GTTACCACCC CCTTAAGTTT GACTTTAGAC 660
CACTGGAAGG ATGTGGAACG ^{>REFMUCGL.GAG 1415}GACAGCCAC ACCGTGCGG TAGAGGTTAG AAAAAGCGC 720
TGGGTTACAT TCTGCTCTGC AGAATGGCCA ACCTCAACG TCGATGGCC ACGAGACGC 780
ACTTTTAACC CAGACATTAT TACACAGGT AAGATCAAGG TCCTCTCACC TGGCCACAT 840
GGACATCCGG ATCAGGTCCC CTACATCGTG ACCTGGGAAG CTATAGCAGT AGACCCCTT 900
CCCTGGGTCA GACCCCTCGT GCACCCTAA CCTCCCTCT CTCTTCCCC TTCAGCCCC 960
TCTCTCCCAC CTGAACCCC ACTCTGACC CCGCCCCAGT CCTCCCTCTA TCCGCTCTC 1020
ACTTCTCCTT TAAACACCAA ACCTAGGCCT ^{SHI}CAAGTCCTTC CTGATAGCGG AGGACCACTC 1080

^{PR75}
└─┐
GCSA

FIGURE 1b

FIGURE 1c

ATTGATCTAC TCACGGAGGA CCCTCGCCT TACCGGACC CAGGGCCACC CTCTCCTGAC 1140
GGGAACGGCG ATAGCGGAGA AGTGGCCCT ACAGAGGAG CCCCTGACCC TTCCCCAATG 1200
GTATCCGCC TCGGGGGAG AAAAGAACCC CCGTGGCGG ATTCTACTAC CTCTCAGGCG 1260
TTCCCCCTC GCCTGGGAGG GAATGGACAG TATCAATACT GGCCATTTTC CTCCTCTGAC 1320
CTCTATAACT GGAAAAATAA CAACCCCTCT TTCTCCGAGG ACCAGCTAA ATTGACAGCT 1380
TTGATCGAGT CCGTTCTCCT TACTCATCAG CCCACTTGGG ATGACTGCCA ACAGCTATTA 1440
GGGACCTGC TGACGGGAGA AGAAAAACAG CGAGTGCTCC TAGAGGCCCG AAAGGGGTT 1500
CGAGGGGAGG ACGGACGCC AACTCAG GGGGATCTCTAGAGTGCAGCTGCAGGCAAGCT
BamH I Xba I Pst I Hind II Sal I Sph I
Hinc II Acc I
CAGATCCAAT TCGATTAG TTCAATTTGT TAAAGACAGG ATCTCAGTAG 7740
TCCAGGCTTT AGTCCTGACT CAACAATACC ACCAGCTAA ACCACTAGAA TACGAGCCAC 7800
AATAAATAAA AGATTTTATT TAGTTTCCAG AAAAAAGGGG GAATGAAAGA CCCACCAAA 7860
REFMLVCGD. ENV<

FIGURE 1c

TTGCTTAGCC TGATAGCCG AGTAACGCCA TTTTGAAGG CATGGA AAAA TACCAAAACCA 7920
AGAAATAGAGA AGTTCAGATC AAGGGCGGGT ACACGAAAC AGCTAACGTT GGGCCAAACA 7980
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCCCGGGGCC AAGAACAGAT GGTCAACCGG 8040
GTTCCGGCCC GGC CGGGGC CAAGAACAGA TGGTCCCCAG ATATGGCCCC ACCCTCAGCA 8100
GTTTCTT¹AG ACCCATCAGA TGTTC²CAGG CTC³CCCCAAG GACCTGAAAT GACCTGTGC 8160
CTTATTGAA TTAACCAATC AGCCTGCTTC TCGCTTCTGT TCGCGCGGCTT CTGCTTCCCG 8220
AGCTCTATAA AAGAGCTCAC AACCCCTCAC
GGGCCAGTCC TCGGATAGAC TGAGTCGGCC GGTACCCGT GTATCCAATA AATCCTCTTG 60
CTGTTCATC CGACTCGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCAG AGTGATTGAC 120
TACCCGTCTC GGGGTCTTT CATTTGGGG CTGCTCCGG ATCTGGAGAC CCCTGCCCG 180
GGACCACCGA CCCACCACCG EGAGGTAAGC TGGCCAGCAA TTGTTCTGTG TCTGTCCATT 240
GTCTGTGTC TTGATTGAT TTTATGCGCC TGTGTCTGT⁴ CTAGTTGGCC GACTAGATTG 300
GTATCTGGCG GATC T → PUC 19

R
U3
KpnI
SnaI
PstI
BglII
PUC 19

FIGURE 1d

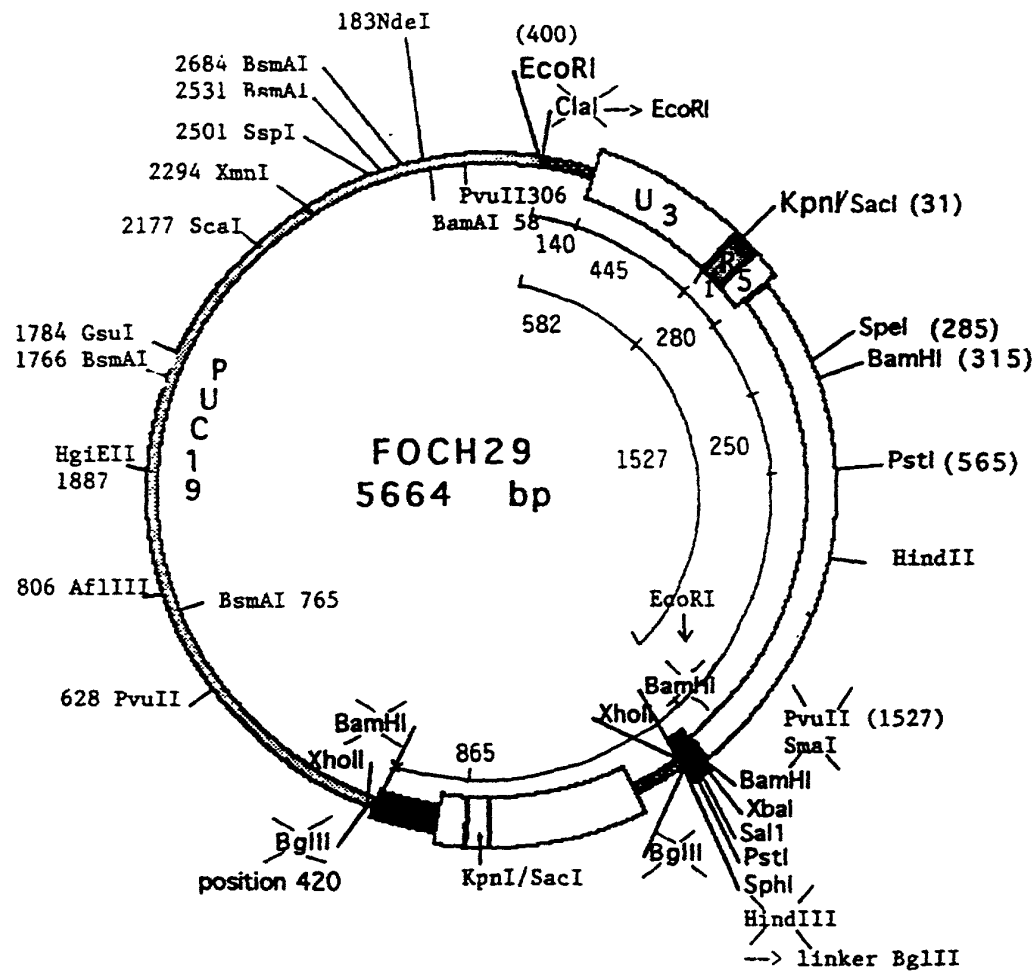
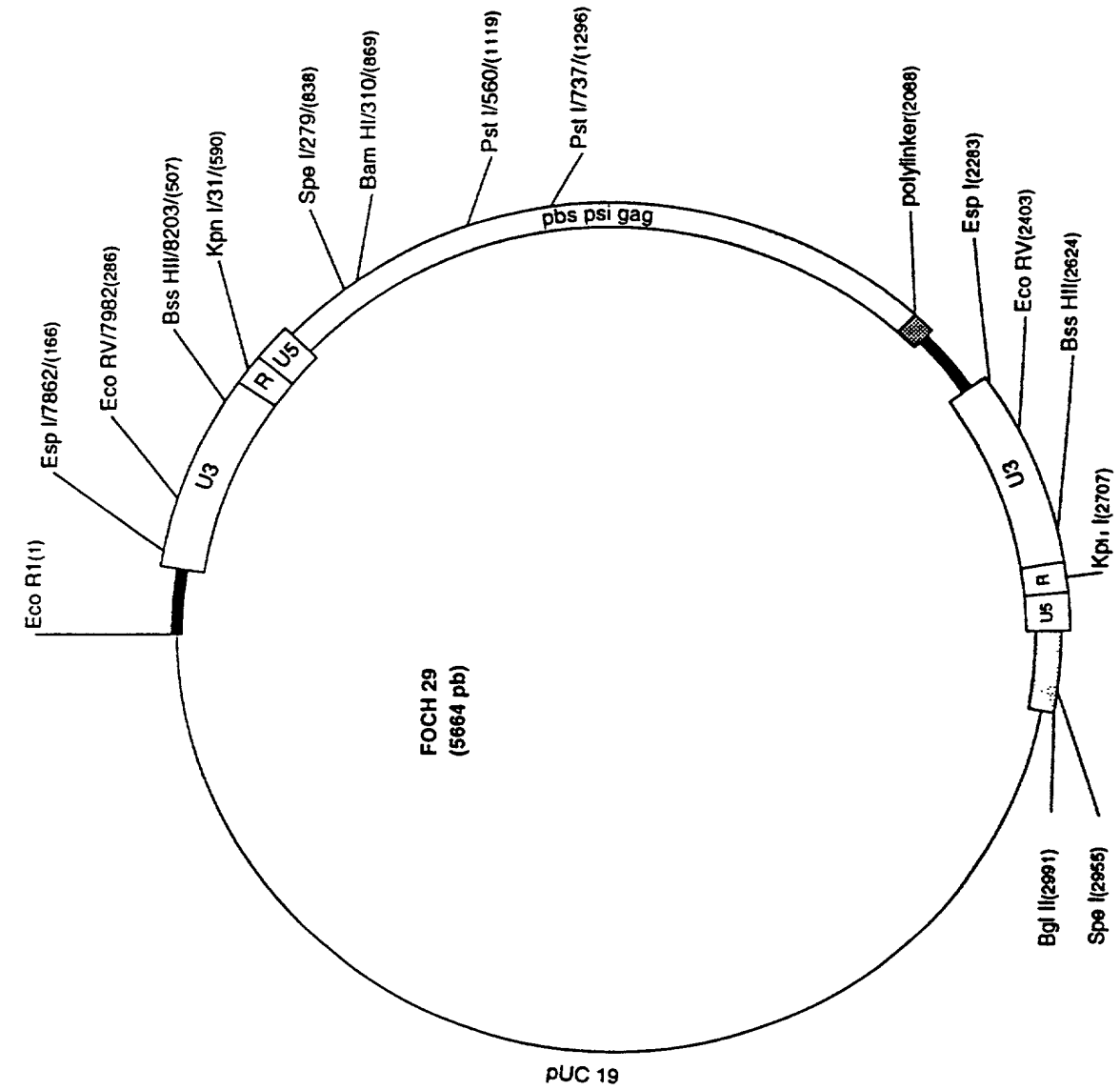


FIGURE 2 A



polylinker
Bam HI : 2088
Xba I : 2094
Sal I : 2100
Pst I : 2106
Sph I : 2112

FIGURE 2B

FOOT 26502660

1134

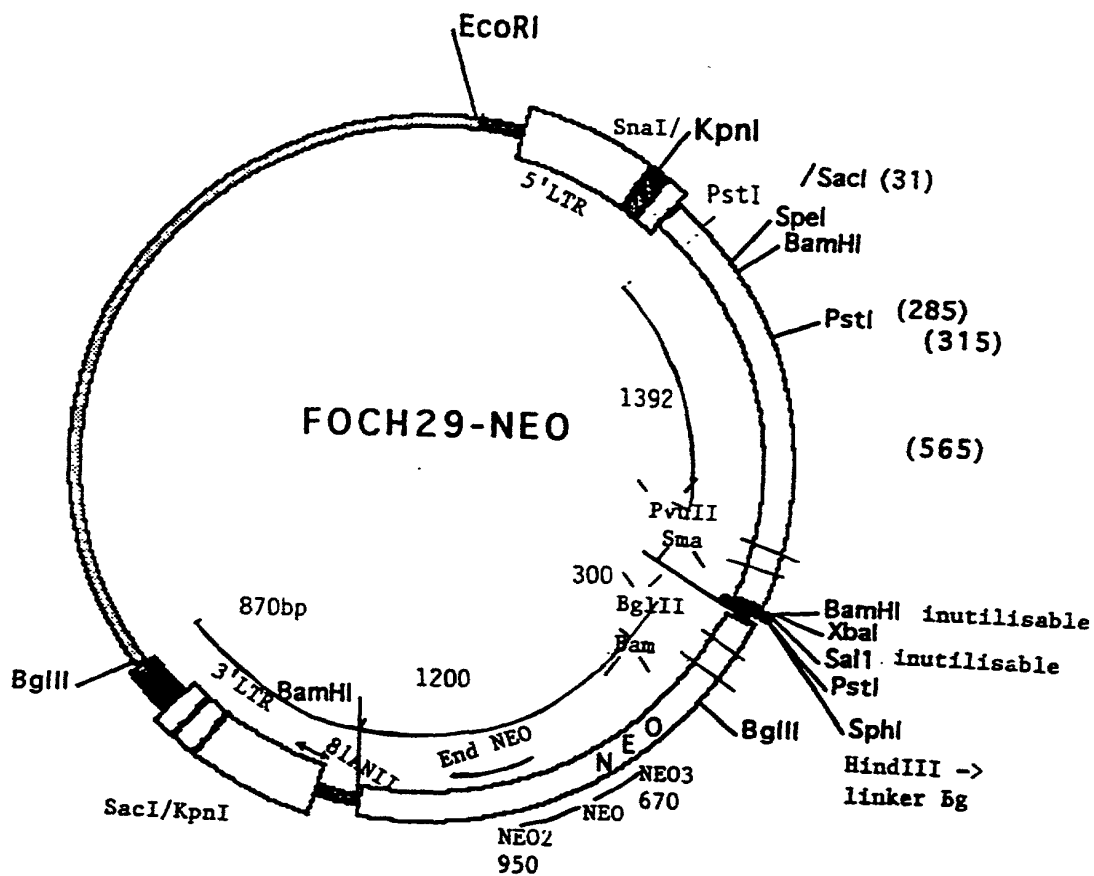


FIGURE 3



1. Yamash-Perron, C., Vieira, J. and Messing, J. (1985) *Gene* 33, 103-119.
2. Genbank Accession # V80026 (Vecbase:pUC19c).

FIGURE 4

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R
 GCGCCAGTCC TCCGATAGAC TGAGTCGCCC KpnI GGGTACCCGT GTATCCAATA AATCCTCTTG 60
 CTGTTGCATC CGACTCGTGG TCTCGCTGTT SmaI CCTTGGGAGG GTCTCCTCAG AGTGATTGAC 120
 TACCCGTCTC GGGGGTCTTT TR CATTGGGGG PBS CTCGTCCGGG ATCTGGAGAC CCCTGCCCAG 180
 GGACCACCGA CCCACCACCG SD GGAGGTAAGC TGGCCAGCAA TTGTTCTGTG TCTGTCCATT 240
 GTCCTGTGTC TTTGATTGAT TTTATGCGCC Spel TGTGTCTGTA CTAGTTGGCC GACTAGATTG 300
 GTATCTGGCG BamHI GATCCGTGGT GGAAGTACG AGTTCGAGAC ACCCGGCCGC Pr75 GCSA AACCCTGGGA 360
 GACGTCCCGA GGACTTCGGG GGCCATTTTT GTGGCCCGGC CAGAGTCCAA CCATCCCGAT 420
 CGTTTTGGAC TCTTTGGTGC ACCCCCCTTA GAGGAGGGGT ATGTGGTTCT GGTAGGAGAC 480
 AGAGGGCTAA AACGGTTTCC GCCCCGTCT GAGTTTTTGC TTTCGGTTTG GAACCGAAGC 540
 CGCGCCGCGC GTCTTGTCTG PstI CTGCAGCATC GTTCTGTGTT GTCTCTGTTT GACTGTTTTT 600
 CTGTATTTGT CTGAAAACAT GGGCCAGGCT GGTACCACCC CTTAAGTTT GACTTTAGAC 660
 CACTGGAAGG ATGTCGAACG REPMLVCGD.GAG Map15 GACAGCCAC AACCTGTCGG TAGAGGTTAG AAAAAGGCGC 720
 TGGGTTACAT TCTGCTCTGC AGAATGGCCA ACCTTCAACG TCGGATGGCC ACGAGACGGC 780
 ACTTTTAACC CAGACATTAT TACACAGGTT AAGATCAAGG TCTTCTCACC TGGCCACAT 840
 GGACATCCGG ATCAGGTCCC CTACATCGTG ACCTGGGAAG CTATAGCAGT AGACCCCCCT 900
 CCCTGGGTCA GACCCCTCGT GCACCCTAAA CCTCCCCTCT CTCTTCCCCC TTCAGCCCCC 960
 TCTCTCCAC CTGAACCCCC ACTCTCGACC CCGCCCCAGT Map15 pp12 CCTCCCTCTA TCCGGCTCTC 1020
 ACTTCTCCTT TAAACACCAA Stul CAAGTCCTTC CTGATAGCGG AGGACCACTC 1080
 ATTGATCTAC TCACGGAGGA CCCTCCGCCT TACCGGGACC CAGGGCCACC CTCTCCTGAC 1140
 GGGAACGGCG ATAGCGGAGA AGTGGCCCCCT ACAGAAGGAG CCCCTGACCC TTCCCCAATG 1200
 GTATCCCGCC TGCGGGGAAG AAAAGAACCC CCCGTGGCGG ATTCTACTAC CTCTCAGGCG 1260
 p12 CAP30 TTCCCCCTTC GCCTGGGAGG GAATGGACAG TATCAATACT GGCCATTTTC CTCCTCTGAC 1320
 CTCTATAACT GGAAAAATAA CAACCCCTCT TTCTCCGAGG ACCCAGCTAA ATTGACAGCT 1380
 TTGATCGAGT CCGTTCTCCT TACTCATCAG CCCACTTGGG ATGACTGCCA ACAGCTATTA 1440
 GGGACCCTGC TGACGGGAGA AGAAAAACAG CGAGTGCTCC TAGAGGCCCG AAAGGCGGTT 1500
 CGAGGGGAGG ACGGACGCCC AACTCAGCTG PvuII CCAATGACA TTAATGATGC TTTTCCCTTG 1560
 GAACGTCCCG ACTGGGACTA (1527) N+B+ CAACACCAA CGAGGTAGGA ACCACCTAGT CCACTATCGC 1620
 CAGTTGCTCC TAGCGGGTCT CCAAAACGCG GGCAGAAGCC CCACCAATTT GGCCAAGGTA 1680
 AAAGGGATAA CCCAGGGACC TAATGAGTCT CCCTCAGCCT TTTTAGAGAG ACTCAAGGAG 1740
 GCCTATCGCA GATACTCTCC TTATGACCCT GAGGACCCAG GGCAAGAAAC CAATGTGGCC 1800

FIGURE 5A

FIGURE 5B

11/26

09970597 1004001
GCCCTGGGAT TGCCAGACTT GACTAAGCCC TTCGAACTTT TTGTTGACGA GAAGCAGGGC 3720
TACGCCAAAG GTGTCCTAAC GCAAAACTG GGGCCTTGCC GTCCGGCCGGT GGCCTACCTG 3780
TCCAAAAAGC TAGACCCAGT GGCAGCTGGG TGGCCCCCTT GCCTACGGAT GGTAGCAGCC 3840
ATCGCCGTTT TGACCAAAGA CGCTGGCAAG CTCACCATGG GACAGCCACT AGTCATTCTG 3900
GCCCCCATG CAGTAGAGGC ACTAGTTAAG CAACCCCCTG ATCGCTGGCT CTCCAACGCC 3960
CGAATGACCC ACTACCAGGC TCTGCTTCTG GACACGGACC GAGTCCAGTT CGGACCAATA 4020
GTGGCCCTAA ACCCAGCTAC GCTGCTCCCT CTACCTGAGG AGGGGCTGCA ACATGACTGC 4080
CTTGACATCT TGGCTGAAGC CCACGGAAT AGACCAGATC TTACGGACCA GCCTCTCCCA 4140
GACGCTGACC ACACCTGGTA CACAGATGGG AGCAGCTTCC TGCAAGAGGG GCAGCGCAAG 4200
GCCGGAGCAG CAGTAACCAC CGAGACCGAG GTAGTCTGGG CCAAAGCACT GCCAGCCGGG 4260
ACATCGGCCC AAAGAGCTGA GTTGATAGCG CTCACCCAAG CCTTAAAAAT GGCAGAAGGT 4320
AAGAAGCTGA ATGTTTACAC CGATAGCCGT TATGCTTTTG CCACTGCCCCA TATTCACGGA 4380
GAAATATATA GAAGGCGCGG GTTGCTCACA TCAGAAGGAA AAGAAATCAA AAATAAGGAC 4440
GAGATCTTGG CCCTACTGAA GGCTCTCTTC CTGCCCAAAA GACTTAGCAT AATTCATTGC 4500
CCGGGACATC AGAAGGGAAA CCGCGCGGAG GCAAGGGGCA ACAGGATGGC CGACCAAGCG 4560
GCCCAGAGAAG TAGCCACTAG AGAACTCCA GAGACTTCCA CACTTCTGAT AGAAAATTCA 4620
GCCCCCTATA CTCATGAACA TTTTCACTAT ACGGTGACTG ACATAAAAGA TCTGACTAAA 4680
CTAGGGGCCA CTTATGACGA TGCAAAGAAG TGTGGGTTT ATCAGGGAAA GCCTGTAATG 4740
CCTGATCAAT TCACCTTTGA ACTATTAGAT TTTCTTCATC AATTGACCCA CCTCAGTTTC 4800
TCAAAAACAA AGGCTCTTCT AGAAAGGAAC TACTGTCTT ATTACATGCT GAACCGGGAT 4860
CGAACGCTCA AAGACATCAC TGAGACTTGC CAAGCCTGTG CACAGGTCAA TGCCAGCAAG 4920
TCTGCCGTCA AACAAGGGAC TAGAGTTCGA GGGCACCGAC CCGGCACCCA CTGGGAAATT 4980
GATTTCACTG AGGTAAAACC TGGCCTGTAT GGGTATAAAT ATCTTTTAGT TTTCATAGAC 5040
ACTTTCTCTG GATGGGTAGA AGCTTTCCCA ACCAAGAAAG AACTGCCAA AGTTGTAACC 5100
AAGAAGCTAC TAGAAGAAAT CTTCCCCAGA TTCGGCATGC CACAGGTATT GGAACCGAC 5160
AATGGGCCTG CCTTCGTCTC CAAGGTAAGT CAGACAGTAG CCGATTTACT GGGGGTTGAT 5220
TGGAACTAC ATTGTGCTTA CAGACCCAG AGTTCAGGTC AGGTAGAAAG AATGAATAGG 5280
ACAATCAAGG AGACTTTAAC TAAATTGACG CTTGCAACTG GCTCTAGGGA CTGGGTGCTC 5340
CTGCTTCCCC TAGCCCTGTA TCGAGCCCGC AACACGCCGG GCCCCCATGG TCTACCCCA 5400

FIGURE 5C

TATGAAATCT TATATGGGGC ACCCCCGCCC CTTGTAAACT TCCCTGATCC TGACATGGCA 5460
AAGGTTACTC ATAACCCCTC TCTCCAAGCC CATTTACAGG CACTCTACCT GGTCCAGCAC 5520
GAAGTCTGGA GACCGTTGGC GGCAGCTTAC CAAGAACAAC TGGACCGGCC GGTAGTGCCT 5580
CACCCCTTTC GAGTCGGTGA CACAGTGTGG GTCCGCAGAC ACCAAACTAA AAATCTAGAA 5640
CCCCGCTGGA AAGGACCTTA TACCGTCCTA CTGACTACCC CCACCGCTCT CAAAGTGGAC 5700
GGCATTGCAG CGTGGATCCA CGCTGCCCAC GTAAAGGCTG CCGACACCAG GATTGAGCCA 5760

CCATCGGAAT CGACATGGCG TGTTCAACGC TCTCAAAATC CCCTAAAGAT AAGATTGACC 5820
>REFMLVCGD. ENV
CGCGGGACCT CTAATCCCC TTAATTCTCT TCCTGTCTCT CAAAGGGGCC AGATCCGCAG 5880
REFMLVCGD. POL<
CACCCGGCTC CAGCCCTCAC CAGGTCTACA ACATTACCTG GGAAGTGACC AATGGGGATC 5940
GGGAGACAGT ATGGGCAATA TCAGGCAACC ACCCTCTGTG GACTTGGTGG CCAGTCCTCA 6000
CCCCAGATTT GTGTATGTTA GCTCTCAGTG GGCCGCCCCA CTGGGGGCTA GAGTATCAGG 6060
CCCCCTATTC CTCGCCCCCG GGGCCCCCTT GTTGCTCAGG GAGCAGCGGG AACGTTGCAG 6120
GCTGTGCCAG AGACTGCAAC GAGCCCTTGA CCTCCCTCAC CCCTCGGTGC AACACTGCCT 6190
GGAACAGACT TAAGCTGGAC CAGGTAACCT ATAAATCAAG TGAGGGATTT TATGTCTGCC 6240
CCGGGTCACA TCGCCCCCGG GAAGCCAAGT CCTGTGGGGG TCCAGACTCC TTCTACTGTG 6300
CCTCTTGGGG CTGCGAGACA ACCGGTAGAG TATACTGGAA GCCCTCCTCT TCTTGGGACT 6360
ACATCACAGT AGACAACAAT CTCACCTCTA ACCAGGCTGT TCAGGTATGC AAAGACAATA 6420
AGTGGTGCAA TCCCTTGGCT ATCCGGTTTA CAAACGCCGG GAAACAGGTC ACCTCATGGA 6480
CAACTGGACA CTATTGGGGT CTACGTCTTT ATGTCTCTGG ACAGGACCCA GGGCTTACTT 6540
TCGGGATCCG ACTCAGTTAT CAAAATCTAG GACCTCGGAT CCAATAGGA CCAAACCCCG 6600
TCCTGGCAGA CCAACTTTTCG TTCCCGCTAC CTAATCCCCT ACCCAAACCT GCCAAGTCTC 6660
CCCCCGCCTC TAGTTCGACT CCCACATTGA TTTCCCCGTC CCCCCTCCC ACTCAGCCCC 6720
CGCCAGCAGG AACGGGAGAC AGATTACTAA ATCTAGTACA GGGAGCTTAC CAGGCACTCA 6780
ACCTTACCAA CCCTGATAAA ACTCAAGAGT GCTGGTTATG CCTAGTGTCT GGACCCCCCT 6840
ATTACGAGGG GGTGCGCGTC CTAGGTACTT ATTCCAACCA TACCTCTGCC CCAGCTAACT 6900
GCTCCGTGGC CTCCCAACAC AAGCTGACCC TGTCCGAAGT GACTGGACGG GGACTCTGCA 6960
TAGGAACAGT CCCAAAACT CACCAGGCCC TGTGCAACAC TACCCTTAAG GCAGGCAAAG 7020
GGTCTTACTA TCTAGTTGCC CCCACAGGAA CTATGTGGGC ATGTAACACT GGACTCACTC 7080
CATGCCTATC TGCCACCGTG CTTAATCGCA CCACTGACTA TTGCGTTCTC GTGAATTAT 7140

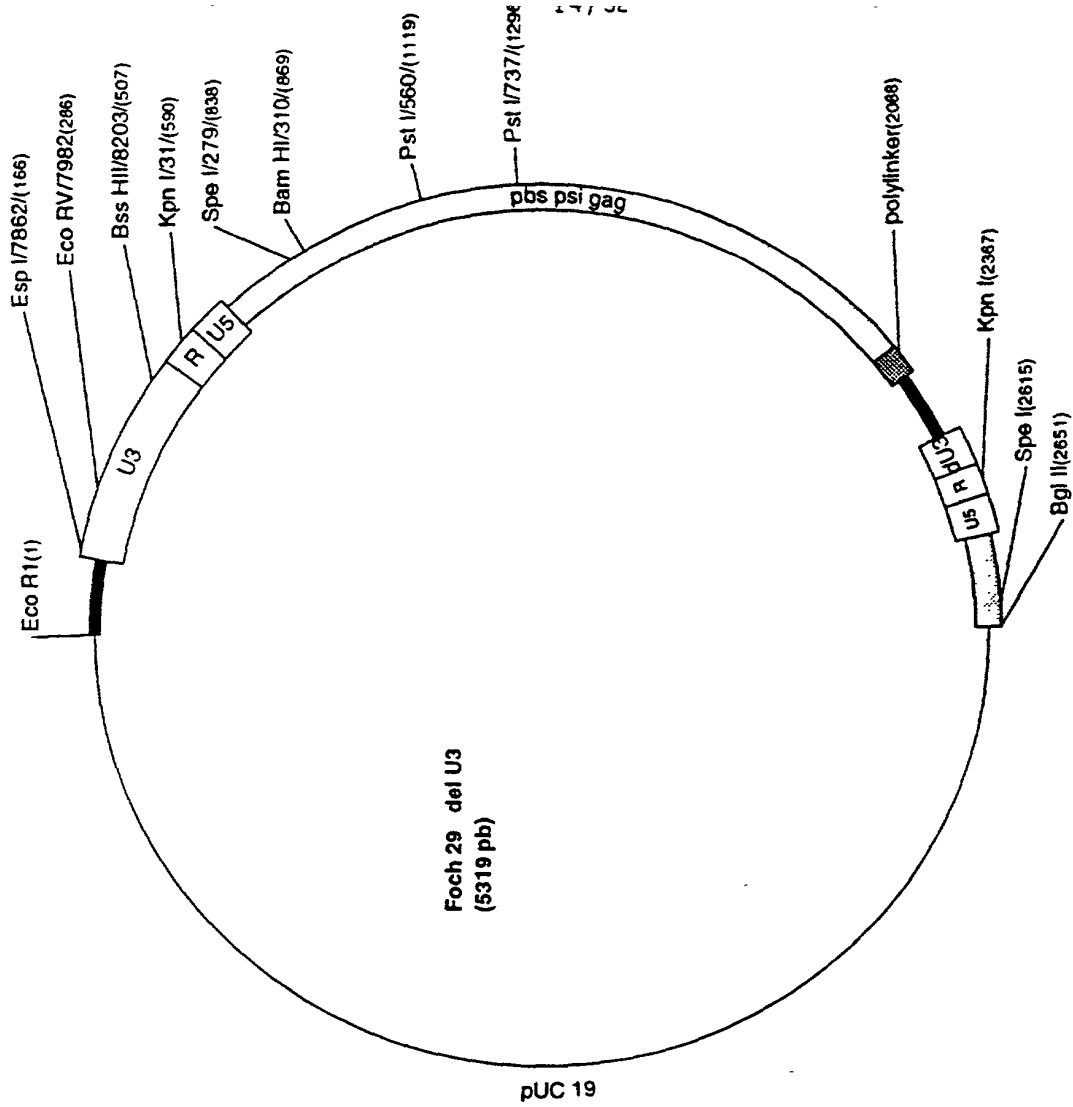
FIGURE 5D

09970597-100404

GGCCCAGGGT CACCTACCAT CCTCCCAGTT ACGTCTATAG CCAGTTTGAA AAATCCCATA 7200
GACATAAAAG AGAACCAGTG TCCTTAACCT TGGCCTTATT ATTAGGTGGG CTAACCTATGG 7260
GTGGCATCGC CGCGGGAGTA GGGACAGGAA CTACCGCCCT GGTGCGCCACC CAGCAGTTTC 7320
AGCAGCTCCA TGCTGCCGTA CAAGATGATC TCAAAGAAGT CGAAAAGTCA ATTACTAACC 7380
TAGAAAAGTC TCTTACTTCG TTGTCTGAGG TTGTA CTGCA GAATCGACGA GGCCTAGACC 7440
TGTTGTTCCCT AAAAGAGGGA GGACTGTGTG CTGCCCTAAA AGAAGAATGT TGTCTCTATG 7500
CTGACCATAC AGGCCTAGTA AGAGATAGTA TGGCCAAATT AAGAGAGAGA CTCTCTCAGA 7560
GACAAAACT ATTTGAGTCG AGCCAAGGAT GGTTCGAAGG ATGGTTTAAAC AGATCCCCCT 7620
GGTTTACCAC GTTGATATCC ACCATCATGG GGCCTCTCAT TATACTCCTA CTAATTCTGC 7680
TTTTTGACC CTGCATTCTT AATCGATTAG TTCAATTTGT TAAAGACAGG ATCTCAGTAG 7740
TCCAGGCTTT AGTCCTGACT CAACAATACC ACCAGCTAAA ACCACTAGAA TACGAGCCAC 7800
AATAAATAAA AGATTTTATT TAGTTTCCAG AAAAAGGGGG GAATGAAAGA CCCCACCAA 7860
TTGCTTAGCC TGATAGCCGC AGTAACGCCA TTTTGCAAGG CATGGAAAAA TACCAAACCA 7920
LTR 81
AGAATAGAGA AGTTCAGATC AAGGGCGGGT ACACGAAAAC AGCTAACGTT GGGCCAAACA 7980
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCCCGGGGCC AAGAACAGAT GGTACCCGCG 8040
LTR + 282
GTTTCGGCCCC GGCCCGGGGC CAAGAACAGA TGGTCCCCAG ATATGGCCCCA ACCCTCAGCA 8100
U3 R
GTTTCTTAAG ACCCATCAGA TGTTTCCAGG CTCCCCCAAG GACCTGAAAT GACCCTGTGC 8160
CTTATTTGAA TTAACCAATC AGCCTGCTTC TCGCTTCTGT TCGCGCGCTT CTGCTTCCCG 8220
AGCTCTATAA AAGAGCTCAC AACCCTCAC TCGGCGCGCC AGTCCTCCGA TAGACTGAGT 8280
CGCCCGGGTA CCCGTGTATC CAATAAATCC TCTTGCTGTT GCA 8323

FIGURE 5E

0970597-100404



polylinker :
Bam HI : 2088
Xba I : 2094
Sal I : 2100
Pst I : 2106
Sph I : 2112

FIGURE 6

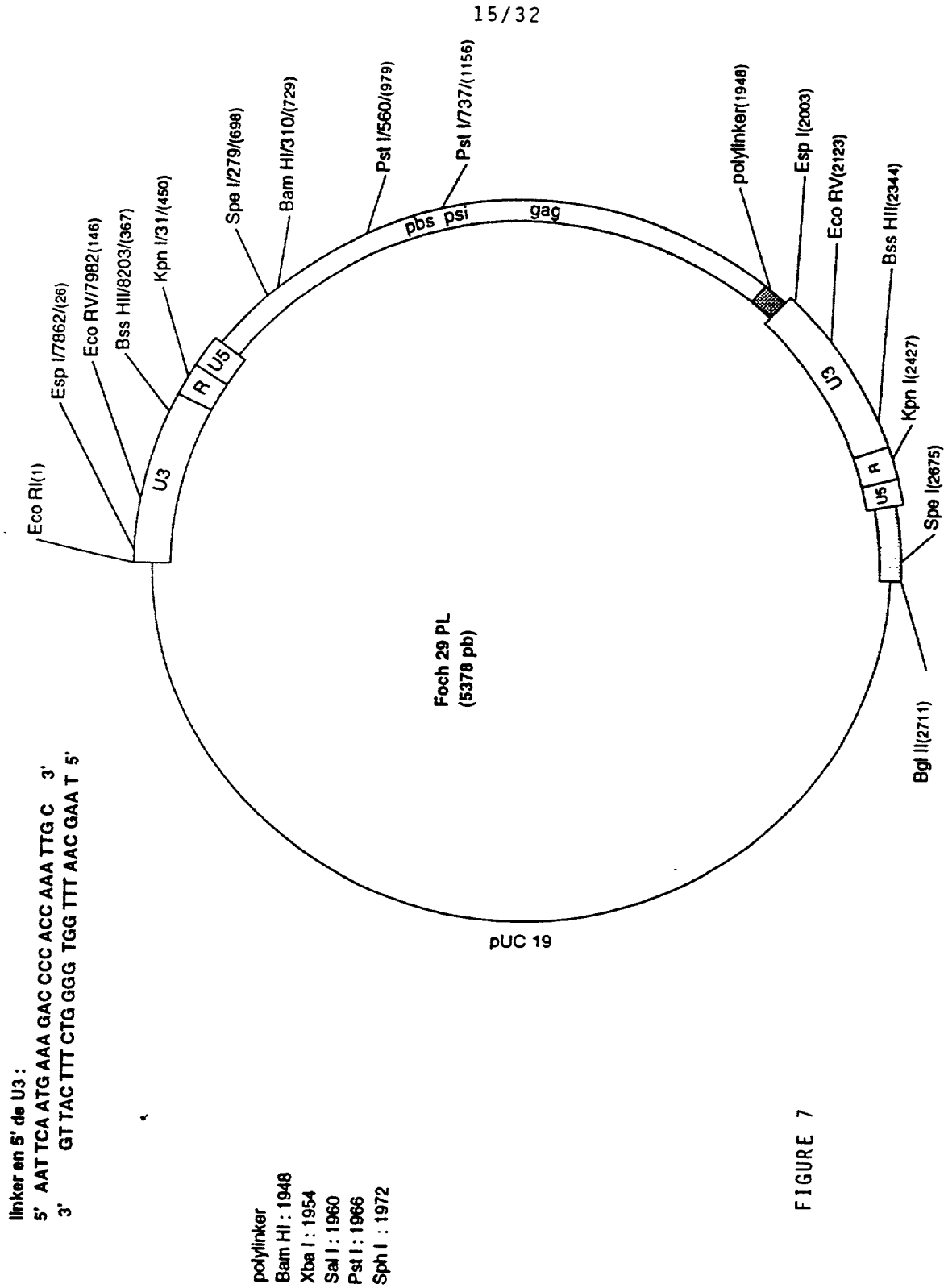


FIGURE 7

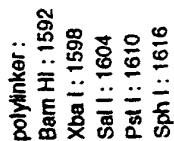


FIGURE 8

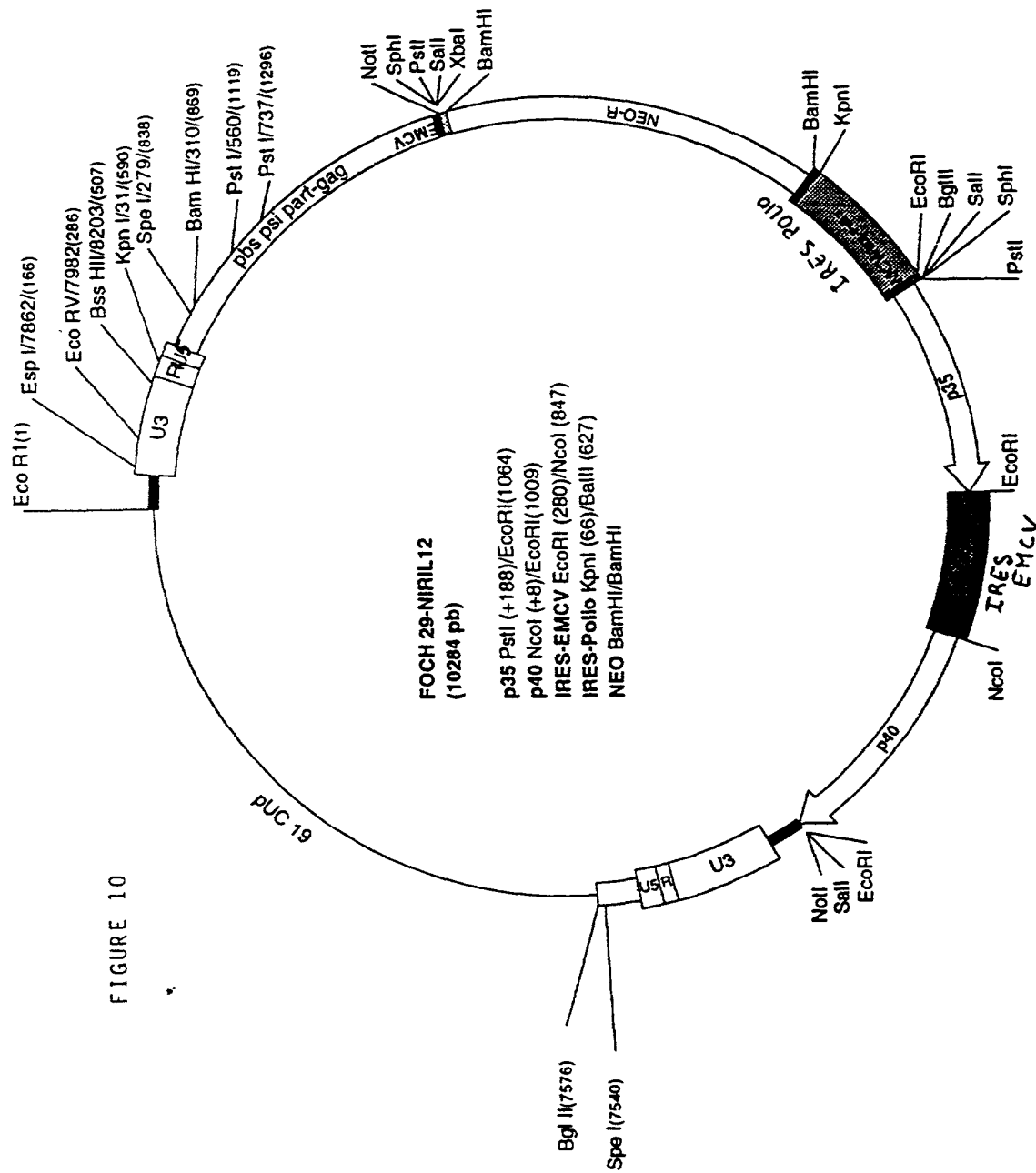
FIGURE 9

The diagram shows a circular plasmid construct labeled "FOCH 29-IL12 (8160 pb)". The construct includes several key elements:

- pUC19**: The origin of replication.
- U3**: A third universal cloning site containing multiple restriction enzyme sites: Eco R1(1), Esp I/7862/(166), Eco RV/7982/(286), Bss HII/8203/(507), Kpn I/31/(590), Spe I/279/(638), Bam HI/310/(669), Pst I/560/(1119), and Pst I/737/(1296).
- gag**: HIV gag gene.
- psi**: HIV psi packaging signal.
- pol**: HIV pol gene.
- ADT8**: A specific HIV target sequence.
- p35**: HIV p35 gene.
- EcoRI**: Restriction site for cloning.
- NcoI**: Restriction site for cloning.
- p40**: HIV p40 gene.
- IRES-EMCV**: Internal Ribosome Entry Site from Encephalomyocarditis virus.
- EcoRI**: Another restriction site for cloning.
- U3**: A second third universal cloning site containing sites: Noll, SalI, and EcoRI.
- Bgl II**: Restriction site at position 5456.
- Spe I**: Restriction site at position 5420.

p35 PsII (+188)/EcoRI(1064)
p40 NcoI (+8)/EcoRI(1009)
IRES-EMCV EcoRI (280)/NcoI

FIGURE 10



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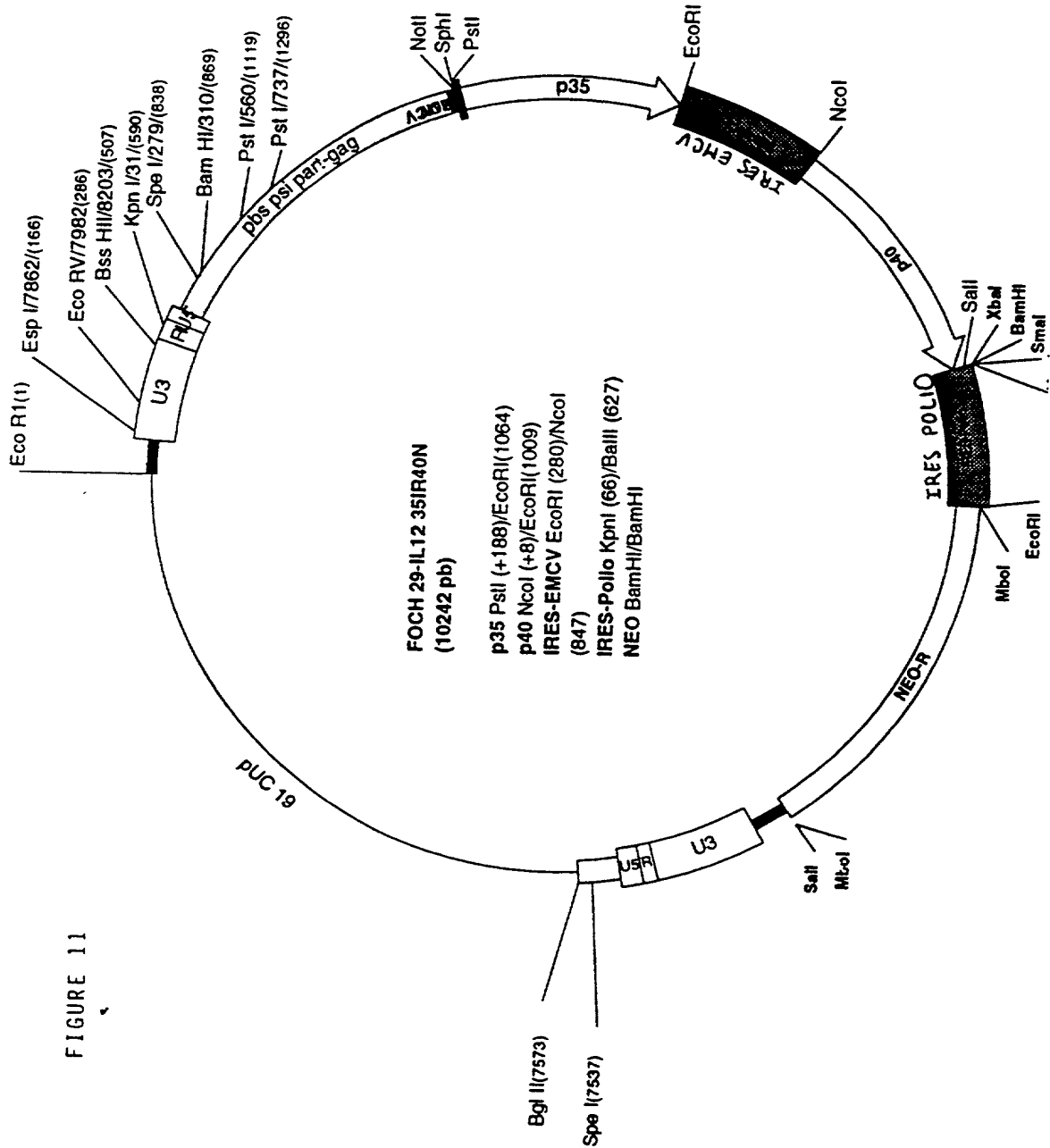
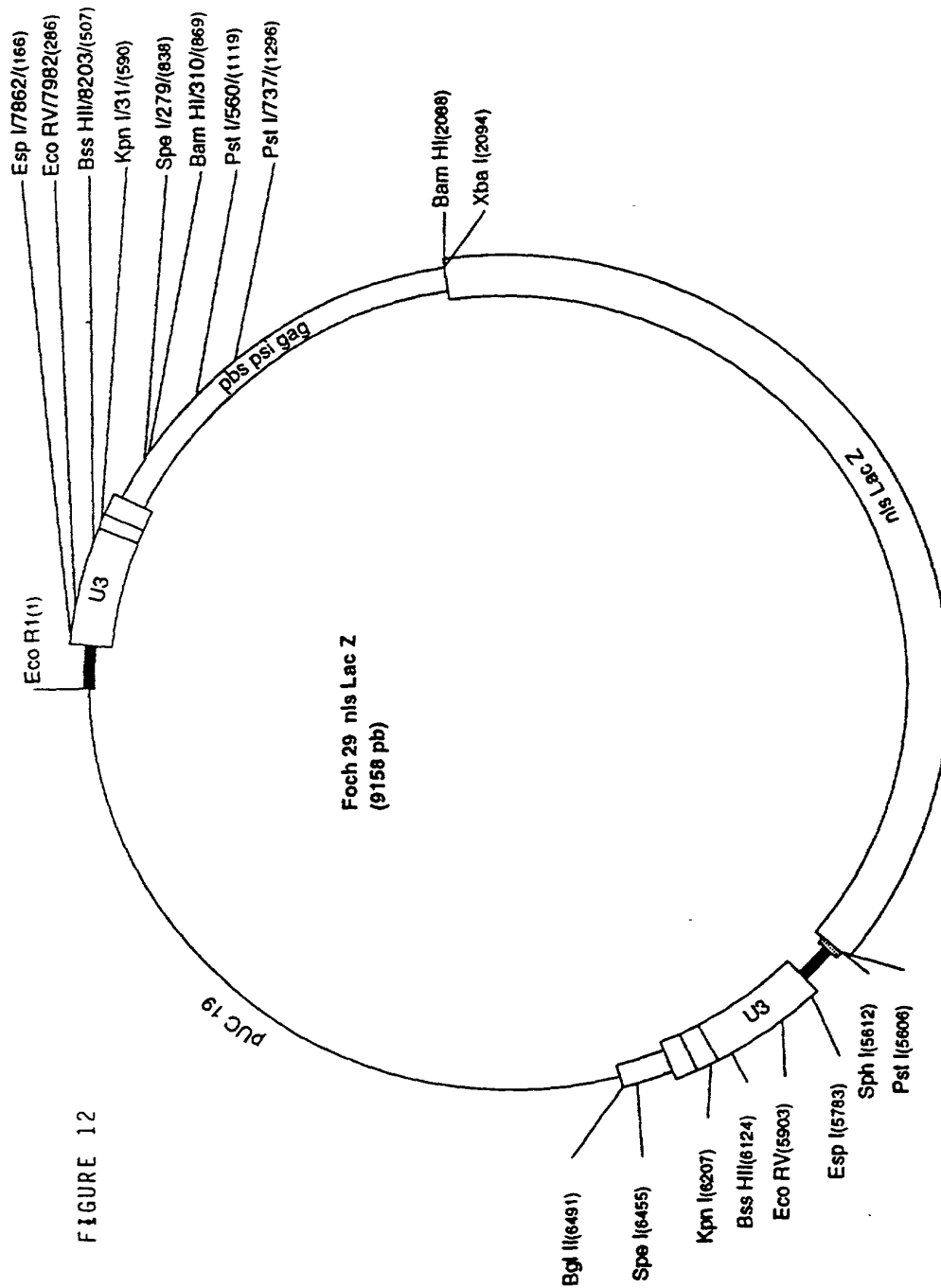


FIGURE 11

FOOT 26502660



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FIGURE 13

FOOT-250460

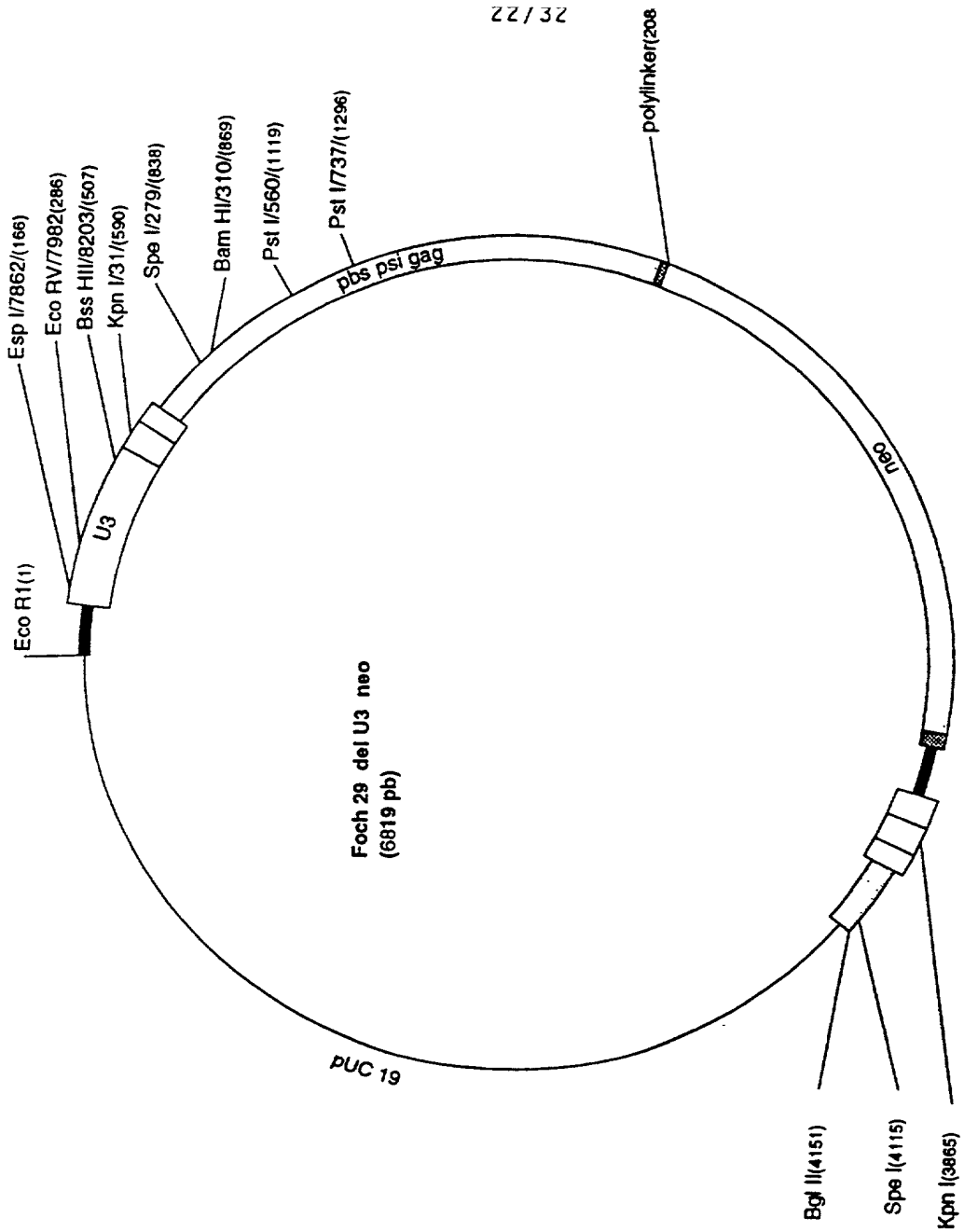


FIGURE 14

FOOT 26502660

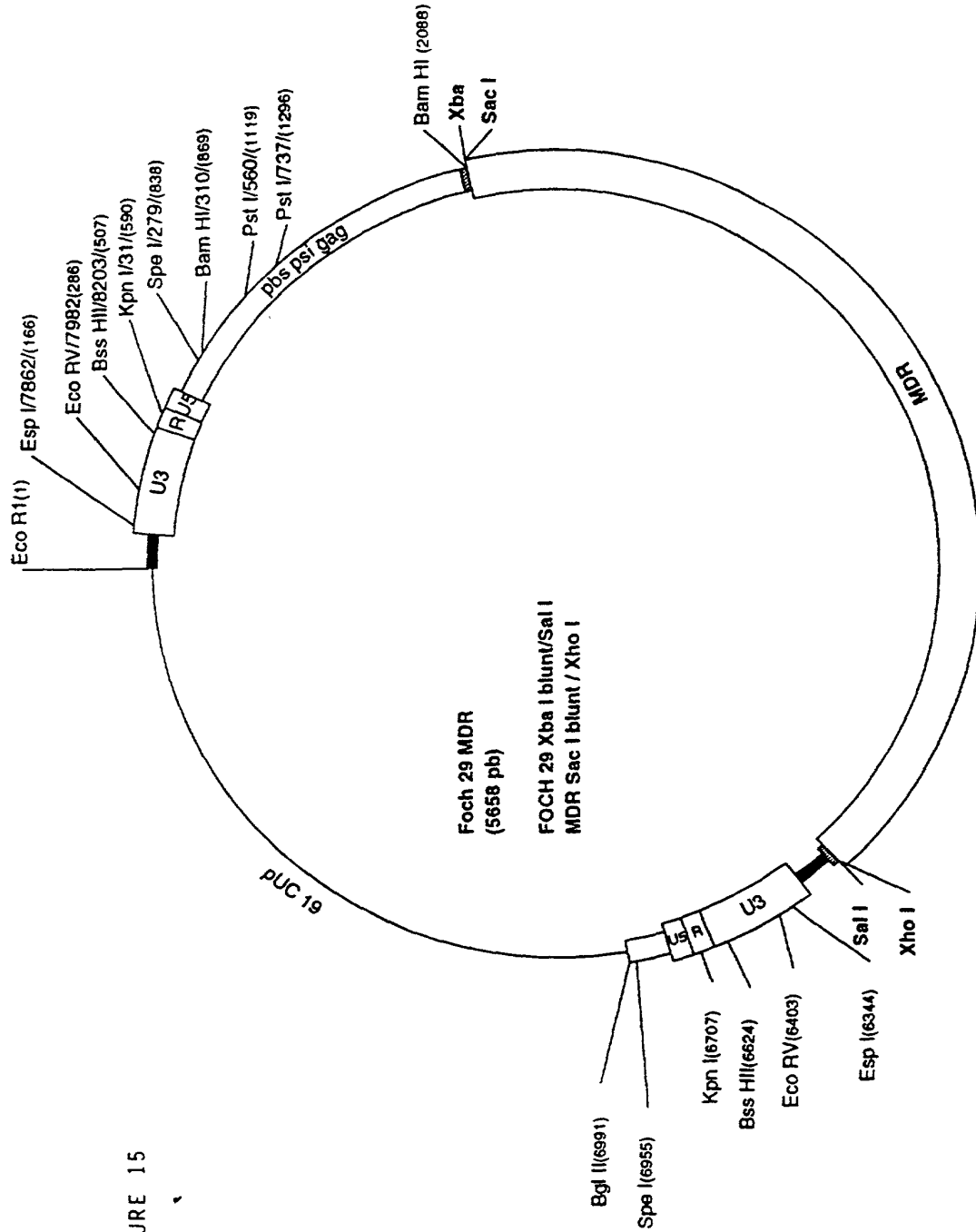
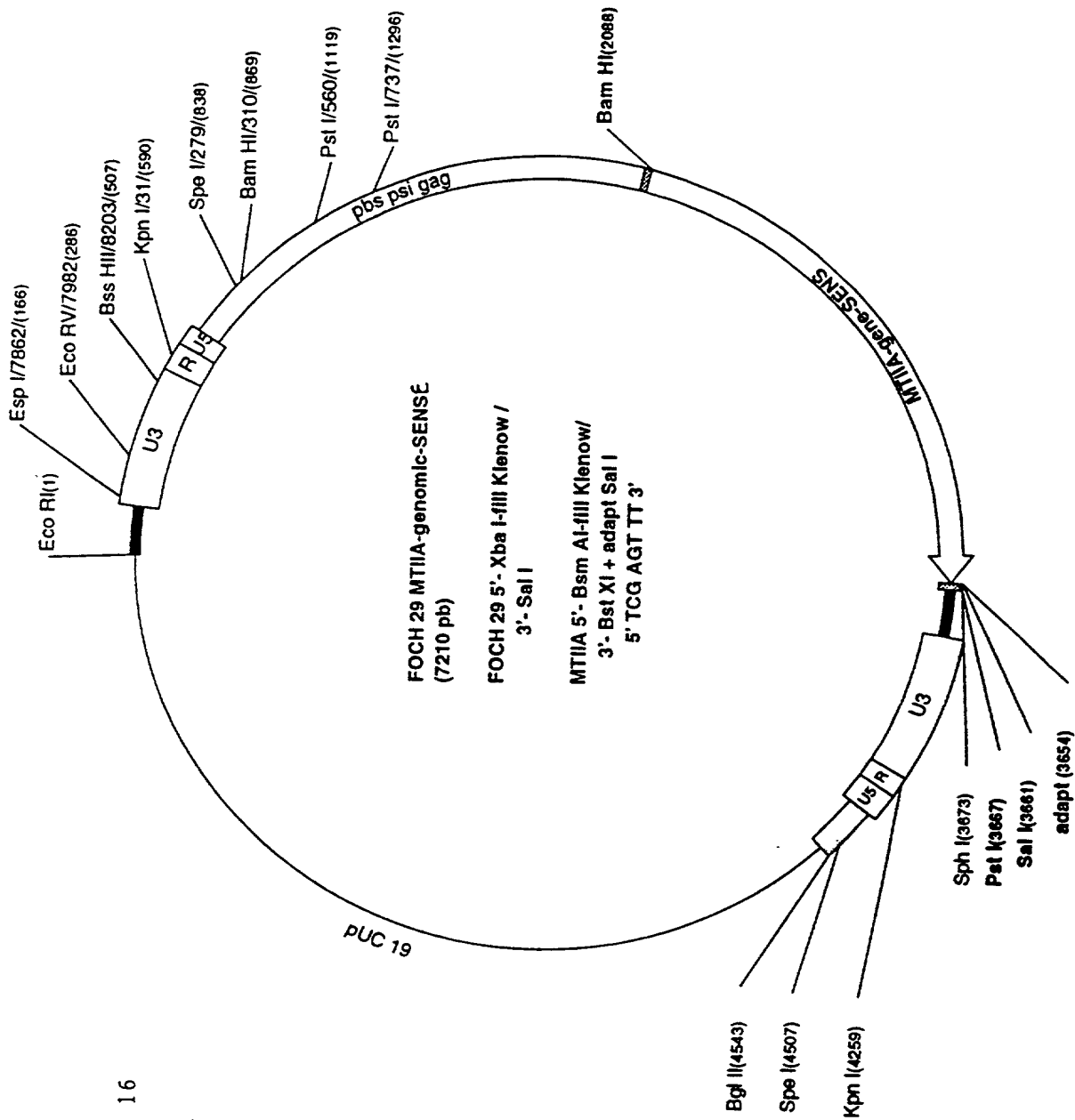


FIGURE 15

Foot 26502550



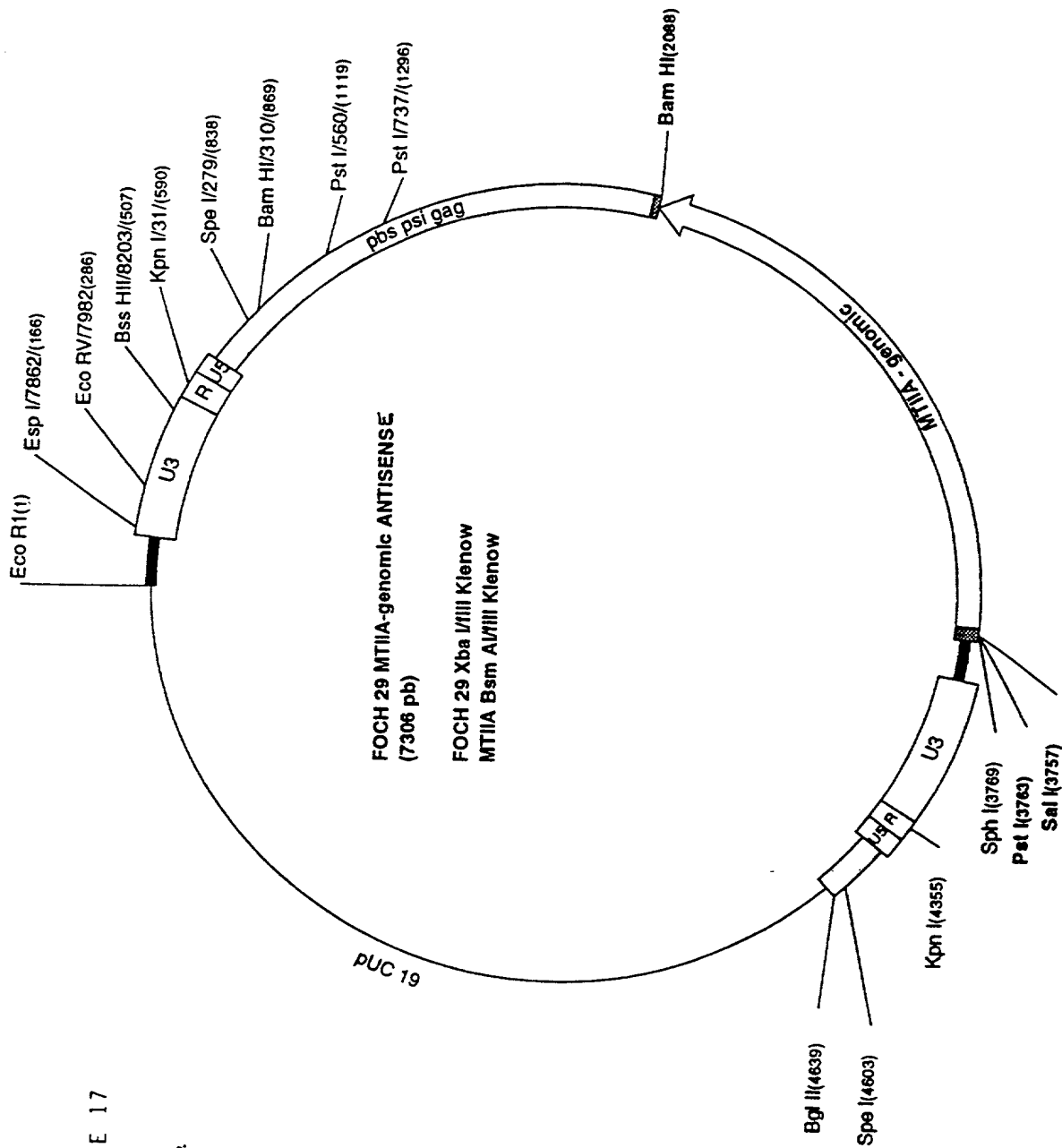
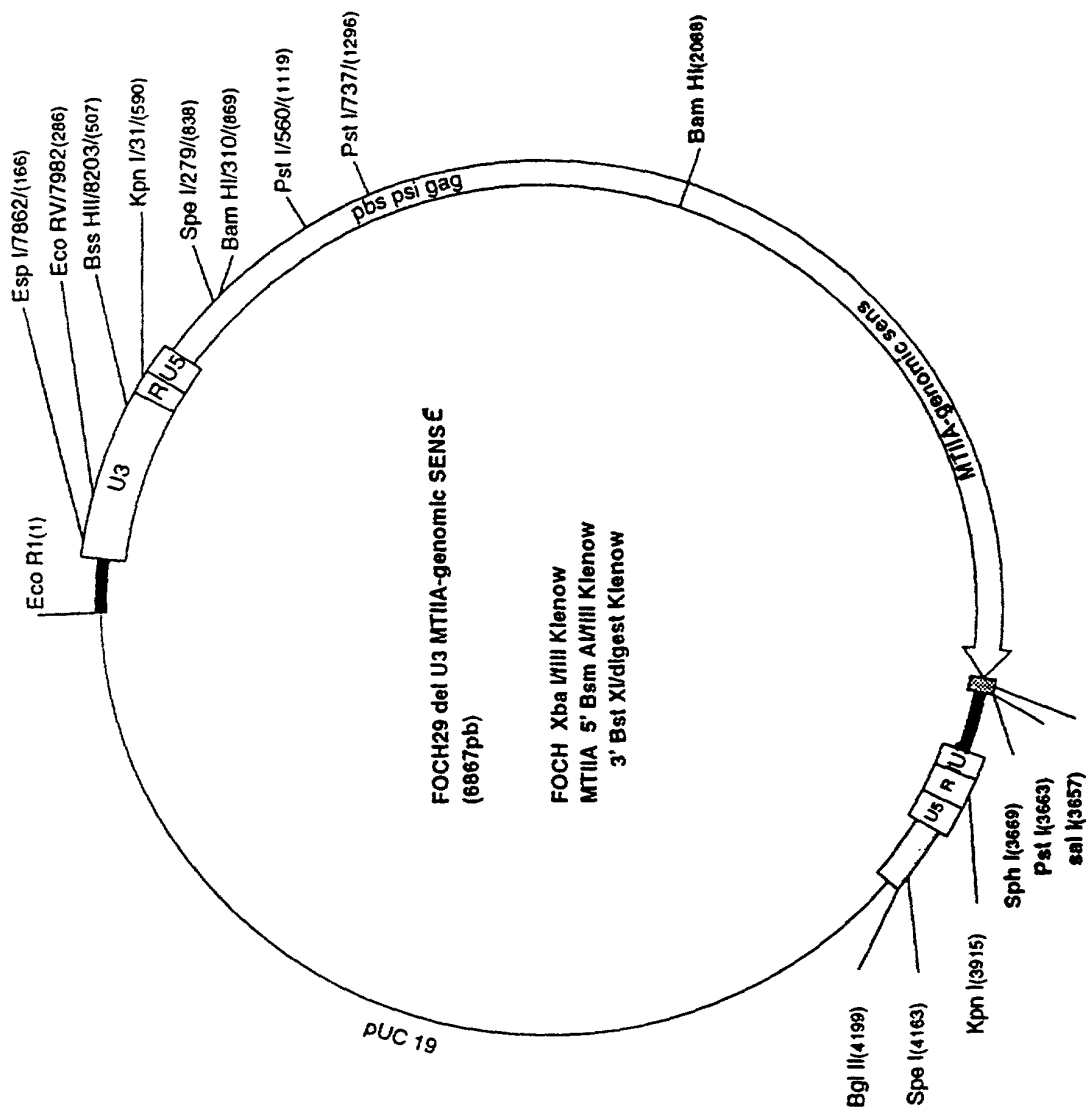
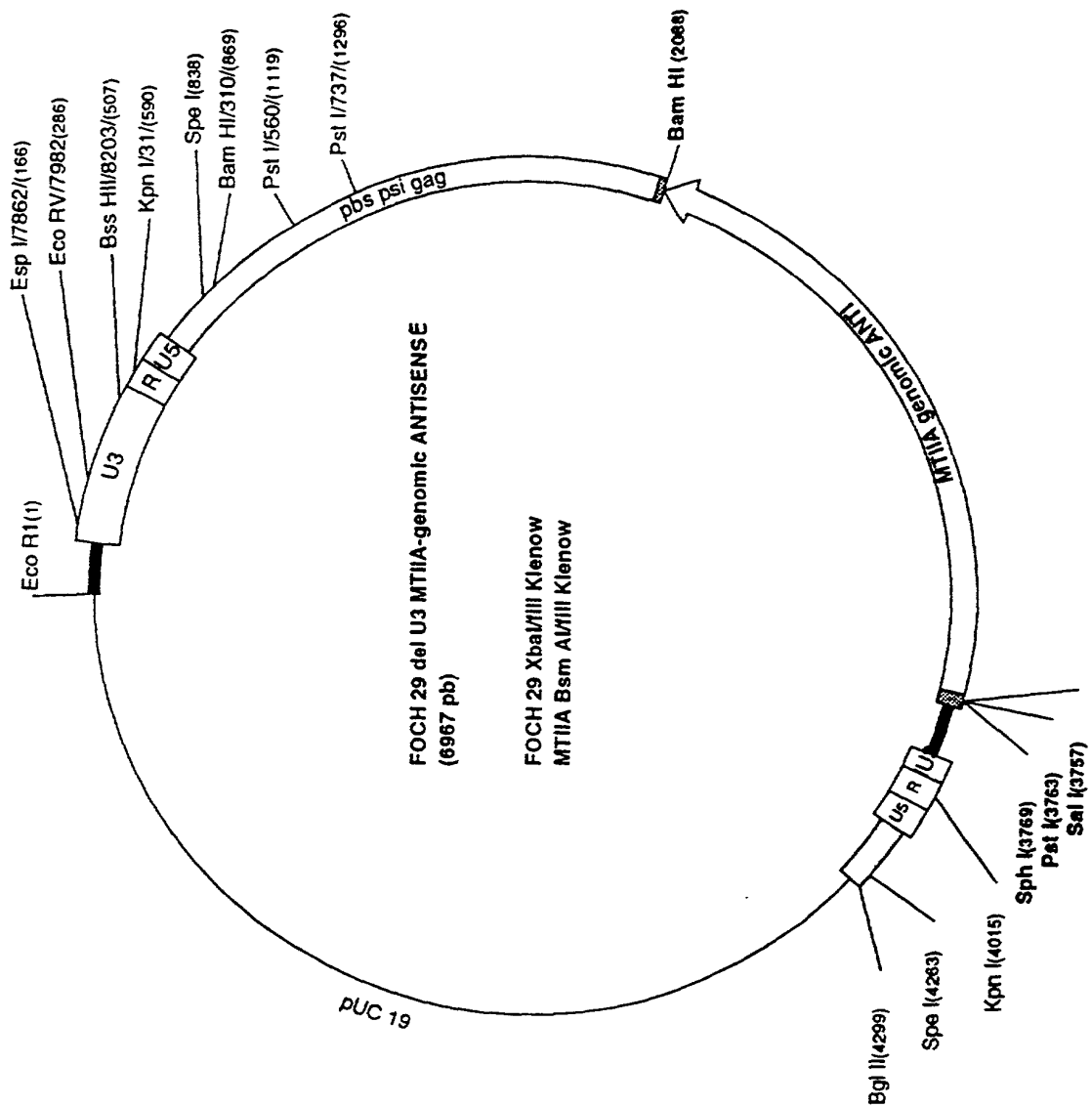


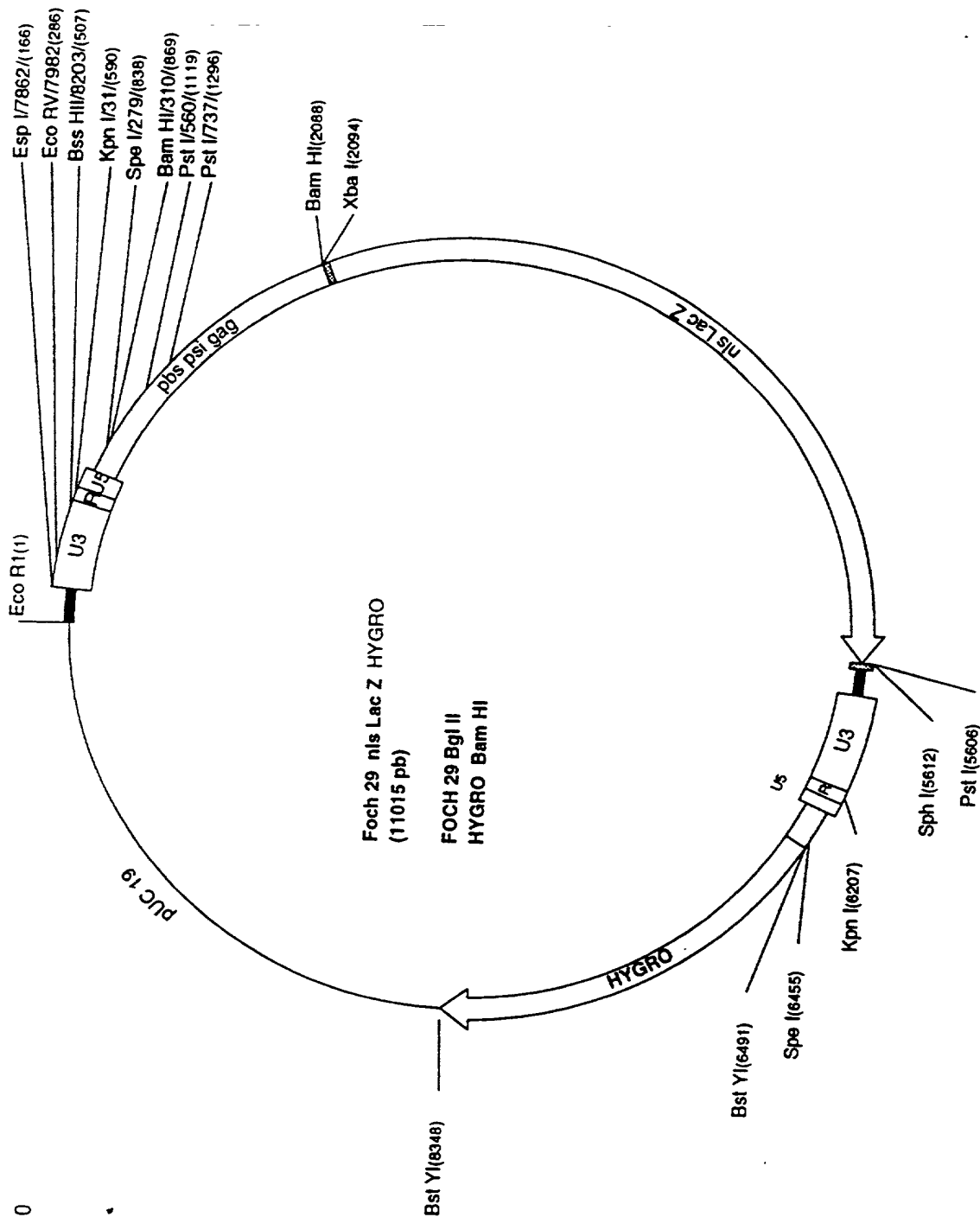
FIGURE 17

FOOT 26504650



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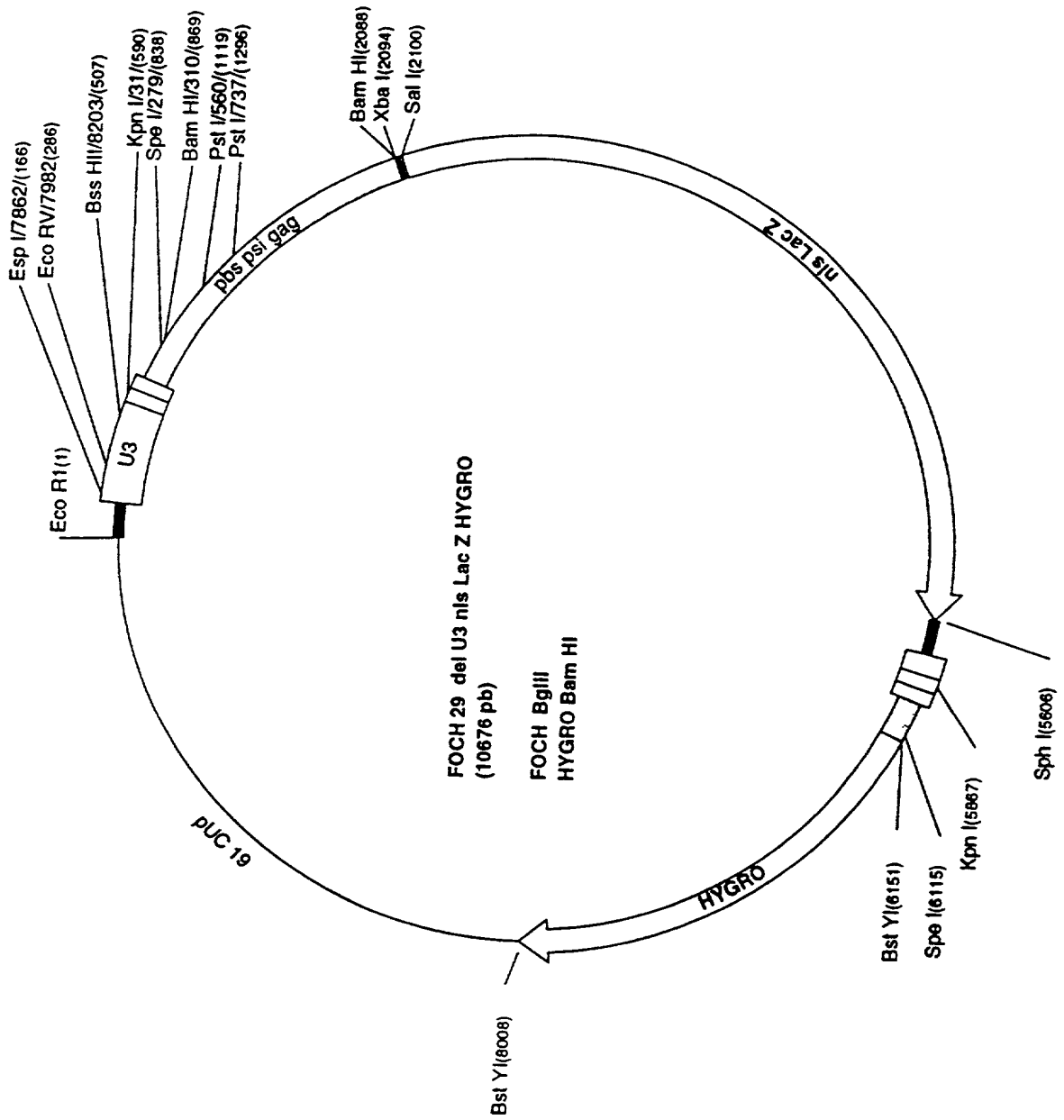
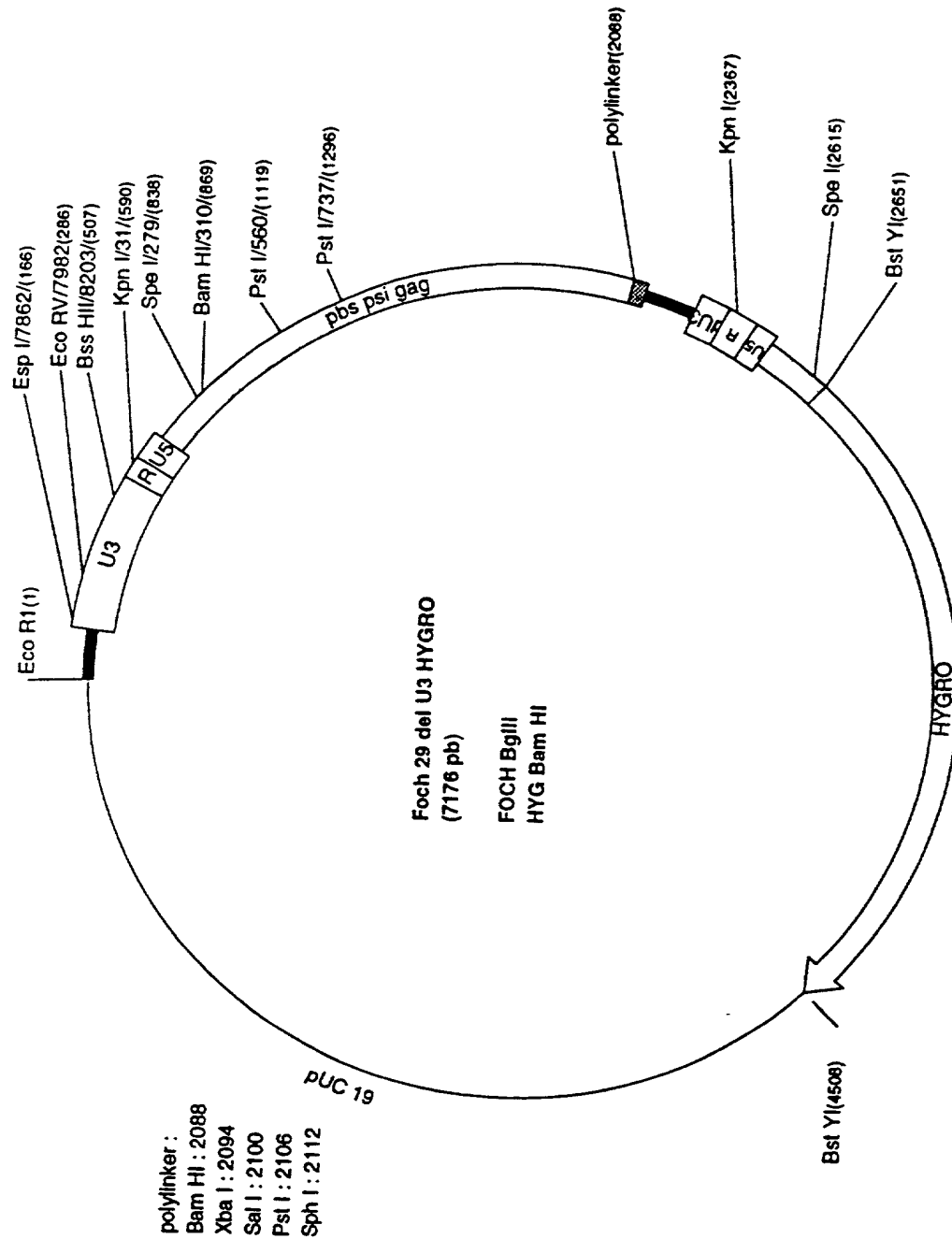


FIGURE 22



1



